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<110> Jing, Shuqian

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Asn	Ile	Thr	Ala	Cys	Lys	Lys	Asn	Glu	Glu	Thr	Val	Glu	Val	Asn	Phe			
				245					250					255				
Thr	Thr	Thr	Pro	Leu	Gly	Asn	Arg	Tyr	Met	Ala	Leu	Ile	Gln	His	Ser			
			260					265					270					
Thr	Ile	Ile	Gly	Phe	Ser	Gln	Val	Phe	Glu	Pro	His	Gln	Lys	Lys	Gln			
		275					280					285						
Thr	Arg	Ala	Ser	Val	Val	Ile	Pro	Val	Thr	Gly	Asp	Ser	Glu	Gly	Ala			
	290					295					300							
Thr	Val	Gln	Leu	Thr	Pro	Tyr	Phe	Pro	Thr	Cys	Gly	Ser	Asp	Cys	Ile			
	305				310					315					320			
Arg	His	Lys	Gly	Thr	Val	Val	Leu	Cys	Pro	Gln	Thr	Gly	Val	Pro	Phe			
				325					330					335				
Pro	Leu	Asp	Asn	Asn	Lys	Ser	Lys	Pro	Gly	Gly	Trp	Leu	Pro	Leu	Leu			
			340					345					350					

Leu Leu Ser Leu Leu Val Ala Thr Trp Val Leu Val Ala Gly Ile Tyr  
355 360 365

Leu Met Trp Arg His Glu Arg Ile Lys Lys Thr Ser Phe Ser Thr Thr  
370 375 380

Thr Leu Leu Pro Pro Ile Lys Val Leu Val Val Tyr Pro Ser Glu Ile  
385 390 395 400

Cys Phe His His Thr Ile Cys Tyr Phe Thr Glu Phe Leu Gln Asn His  
405 410 415

Cys Arg Ser Glu Val Ile Leu Glu Lys Trp Gln Lys Lys Lys Ile Ala  
420 425 430

Glu Met Gly Pro Val Gln Trp Leu Ala Thr Gln Lys Lys Ala Ala Asp  
435 440 445

Lys Val Val Phe Leu Leu Ser Asn Asp Val Asn Ser Val Cys Asp Gly  
450 455 460

Thr Cys Gly Lys Ser Glu Gly Ser Pro Ser Glu Asn Ser Gln Asp Leu  
465 470 475 480

Phe Pro Leu Ala Phe Asn Leu Phe Cys Ser Asp Leu Arg Ser Gln Ile  
485 490 495

His Leu His Lys Tyr Val Val Val Tyr Phe Arg Glu Ile Asp Thr Lys  
500 505 510

Asp Asp Tyr Asn Ala Leu Ser Val Cys Pro Lys Tyr His Leu Met Lys  
515 520 525

Asp Ala Thr Ala Phe Cys Ala Glu Leu Leu His Val Lys Gln Gln Val  
530 535 540

Ser Ala Gly Lys Arg Ser Gln Ala Cys His Asp Gly Cys Cys Ser Leu  
545 550 555 560

<210> 6  
<211> 1713  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (273)..(1427)

<400> 6  
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gctgctaagc ctggccgcgc tgtgcaggag cgccgtaccc cgagagccga ccgttcaatg 120  
tggctctgaa actgggccat ctccagagtg gatgctacaa catgatctaa tcccgggaga 180  
cttgagggac ctccgagtag aacctgttac aactagtgtt gcaacagggg actattcaat 240  
tttgatgaat gtaagctggg tactccgggc ag atg tgg aca ttt tcc tac atc 293  
Met Trp Thr Phe Ser Tyr Ile  
1 5

ggc ttc cct gta gag ctg aac aca gtc tat ttc att ggg gcc cat aat	341
Gly Phe Pro Val Glu Leu Asn Thr Val Tyr Phe Ile Gly Ala His Asn	
10 15 20	
att cct aat gca aat atg aat gaa gat ggc cct tcc atg tct gtg aat	389
Ile Pro Asn Ala Asn Met Asn Glu Asp Gly Pro Ser Met Ser Val Asn	
25 30 35	
ttc acc tca cca ggc tgc cta gac cac ata atg aaa tat aaa aaa aag	437
Phe Thr Ser Pro Gly Cys Leu Asp His Ile Met Lys Tyr Lys Lys Lys	
40 45 50 55	
tgt gtc aag gcc gga agc ctg tgg gat ccg aac atc act gct tgt aag	485
Cys Val Lys Ala Gly Ser Leu Trp Asp Pro Asn Ile Thr Ala Cys Lys	
60 65 70	
aag aat gag gag aca gta gaa gtg aac ttc aca acc act ccc ctg gga	533
Lys Asn Glu Thr Val Glu Val Asn Phe Thr Thr Thr Pro Leu Gly	
75 80 85	
aac aga tac atg gct ctt atc caa cac agc act atc atc ggg ttt tct	581
Asn Arg Tyr Met Ala Leu Ile Gln His Ser Thr Ile Ile Gly Phe Ser	
90 95 100	
cag gtg ttt gag cca cac cag aag aaa caa acg cga gct tca gtg gtg	629
Gln Val Phe Glu Pro His Gln Lys Lys Gln Thr Arg Ala Ser Val Val	
105 110 115	
att cca gtg act ggg gat agt gaa ggt gct acg gtg cag ctg act cca	677
Ile Pro Val Thr Gly Asp Ser Glu Gly Ala Thr Val Gln Leu Thr Pro	
120 125 130 135	
tat ttt cct act tgt ggc agc gac tgc atc cga cat aaa gga aca gtt	725
Tyr Phe Pro Thr Cys Gly Ser Asp Cys Ile Arg His Lys Gly Thr Val	
140 145 150	
gtg ctc tgc cca caa aca ggc gtc cct ttc cct ctg gat aac aac aaa	773
Val Leu Cys Pro Gln Thr Gly Val Pro Phe Pro Leu Asp Asn Asn Lys	
155 160 165	
agc aag ccg gga ggc tgg ctg cct ctc ctc ctg ctg tct ctg ctg gtg	821
Ser Lys Pro Gly Gly Trp Leu Pro Leu Leu Leu Leu Ser Leu Leu Val	
170 175 180	
gcc aca tgg gtg ctg gtg gca ggg atc tat cta atg tgg agg cac gaa	869
Ala Thr Trp Val Leu Val Ala Gly Ile Tyr Leu Met Trp Arg His Glu	
185 190 195	
agg atc aag aag act tcc ttt tct acc acc aca cta ctg ccc ccc att	917
Arg Ile Lys Lys Thr Ser Phe Ser Thr Thr Thr Leu Leu Pro Pro Ile	
200 205 210 215	
aag gtt ctt gtg gtt tac cca tct gaa ata tgt ttc cat cac aca att	965
Lys Val Leu Val Val Tyr Pro Ser Glu Ile Cys Phe His His Thr Ile	
220 225 230	
tgt tac ttc act gaa ttt ctt caa aac cat tgc aga agt gag gtc atc	1013
Cys Tyr Phe Thr Glu Phe Leu Gln Asn His Cys Arg Ser Glu Val Ile	
235 240 245	
ctc gaa aag tgg cag aaa aag aaa ata gca gag atg ggt cca gtg cag	1061
Leu Glu Lys Trp Gln Lys Lys Lys Ile Ala Glu Met Gly Pro Val Gln	
250 255 260	

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tgg ctt gcc act caa aag aag gca gca gac aaa gtc gtc ttc ctt ctt 1109
Trp Leu Ala Thr Gln Lys Lys Ala Ala Asp Lys Val Val Phe Leu Leu
    265                270                275

tcc aat gac gtc aac agt gtg tgc gat ggt acc tgt ggc aag agc gag 1157
Ser Asn Asp Val Asn Ser Val Cys Asp Gly Thr Cys Gly Lys Ser Glu
280                285                290                295

ggc agt ccc agt gag aac tct caa gac ctc ttc ccc ctt gcc ttt aac 1205
Gly Ser Pro Ser Glu Asn Ser Gln Asp Leu Phe Pro Leu Ala Phe Asn
                300                305                310

ctt ttc tgc agt gat cta aga agc cag att cat ctg cac aaa tac gtg 1253
Leu Phe Cys Ser Asp Leu Arg Ser Gln Ile His Leu His Lys Tyr Val
                315                320                325

gtg gtc tac ttt aga gag att gat aca aaa gac gat tac aat gct ctc 1301
Val Val Tyr Phe Arg Glu Ile Asp Thr Lys Asp Asp Tyr Asn Ala Leu
    330                335                340

agt gtc tgc ccc aag tac cac ctc atg aag gat gcc act gct ttc tgt 1349
Ser Val Cys Pro Lys Tyr His Leu Met Lys Asp Ala Thr Ala Phe Cys
    345                350                355

gca gaa ctt ctc cat gtc aag cag cag gtg tca gca gga aaa aga tca 1397
Ala Glu Leu Leu His Val Lys Gln Gln Val Ser Ala Gly Lys Arg Ser
360                365                370                375

caa gcc tgc cac gat ggc tgc tgc tcc ttg tagcccccaccc atgagaagca 1447
Gln Ala Cys His Asp Gly Cys Cys Ser Leu
    380                385

agagacctta aaggcttcct atcccaccaa ttacagggaa aaaacgtgtg atgatcctga 1507

agcttactat gcagcctaca aacagcctta gtaattaaaa cattttatac caataaaaatt 1567

ttcaaatatt gctaactaat gtagcattaa ctaacgattg gaaactacat ttacaacttc 1627

aaagctgttt tatacataga aatcaattac agctttaatt gaaaactgta accattttga 1687

taatgcaaca ataaagcatc ttcagc 1713

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<210> 7  
 <211> 385  
 <212> PRT  
 <213> Homo sapiens

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<400> 7
Met Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val Glu Leu Asn Thr Val
  1                5                10                15

Tyr Phe Ile Gly Ala His Asn Ile Pro Asn Ala Asn Met Asn Glu Asp
    20                25                30

Gly Pro Ser Met Ser Val Asn Phe Thr Ser Pro Gly Cys Leu Asp His
    35                40                45

Ile Met Lys Tyr Lys Lys Lys Cys Val Lys Ala Gly Ser Leu Trp Asp
    50                55                60

Pro Asn Ile Thr Ala Cys Lys Lys Asn Glu Glu Thr Val Glu Val Asn
    65                70                75                80

```

Phe Thr Thr Thr Pro Leu Gly Asn Arg Tyr Met Ala Leu Ile Gln His  
85 95

Ser Thr Ile Ile Gly Phe Ser Gln Val Phe Glu Pro His Gln Lys Lys  
100 105 110

Gln Thr Arg Ala Ser Val Val Ile Pro Val Thr Gly Asp Ser Glu Gly  
115 120 125

Ala Thr Val Gln Leu Thr Pro Tyr Phe Pro Thr Cys Gly Ser Asp Cys  
130 135 140

Ile Arg His Lys Gly Thr Val Val Leu Cys Pro Gln Thr Gly Val Pro  
145 150 155 160

Phe Pro Leu Asp Asn Asn Lys Ser Lys Pro Gly Gly Trp Leu Pro Leu  
165 170 175

Leu Leu Leu Ser Leu Leu Val Ala Thr Trp Val Leu Val Ala Gly Ile  
180 185 190

Tyr Leu Met Trp Arg His Glu Arg Ile Lys Lys Thr Ser Phe Ser Thr  
195 200 205

Thr Thr Leu Leu Pro Pro Ile Lys Val Leu Val Val Tyr Pro Ser Glu  
210 215 220

Ile Cys Phe His His Thr Ile Cys Tyr Phe Thr Glu Phe Leu Gln Asn  
225 230 235 240

His Cys Arg Ser Glu Val Ile Leu Glu Lys Trp Gln Lys Lys Lys Ile  
245 250 255

Ala Glu Met Gly Pro Val Gln Trp Leu Ala Thr Gln Lys Lys Ala Ala  
260 265 270

Asp Lys Val Val Phe Leu Leu Ser Asn Asp Val Asn Ser Val Cys Asp  
275 280 285

Gly Thr Cys Gly Lys Ser Glu Gly Ser Pro Ser Glu Asn Ser Gln Asp  
290 295 300

Leu Phe Pro Leu Ala Phe Asn Leu Phe Cys Ser Asp Leu Arg Ser Gln  
305 310 315 320

Ile His Leu His Lys Tyr Val Val Val Tyr Phe Arg Glu Ile Asp Thr  
325 330 335

Lys Asp Asp Tyr Asn Ala Leu Ser Val Cys Pro Lys Tyr His Leu Met  
340 345 350

Lys Asp Ala Thr Ala Phe Cys Ala Glu Leu Leu His Val Lys Gln Gln  
355 360 365

Val Ser Ala Gly Lys Arg Ser Gln Ala Cys His Asp Gly Cys Cys Ser  
370 375 380

Leu  
385

<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR Primer  
2429-59

<400> 8  
gcagacactg agagcattgt aatcg 25

<210> 9  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR Primer  
1916-83

<400> 9  
ggctcgtatg ttgtgtggaa ttgtgag 27

<210> 10  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR Primer  
2429-56

<400> 10  
atcaagaaga cttccttttc tac 23

<210> 11  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer 1916-80

<400> 11  
tgcaaggcga ttaagttggg taacgccag 29

<210> 12  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Nested PCR  
Primer

<400> 12  
gccgacgggg acgtggatga ac 22

<210> 13  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Nested PCR  
Primer

<400> 13  
catgattacg ccaagctcta atacgactc 29

<210> 14  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Nested PCR  
Primer

<400> 14  
cttcgccgag tgcctgtgca g 21

<210> 15  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Nest PCR  
Primer

<400> 15  
tcacgacgtt gtaaaacgac ggccagtg 28

<210> 16  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR Primer  
2469-50

<400> 16  
gcgatgtcgc tcgtgctgct aag 23

<210> 17  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR Primer  
2469-54

<400> 17  
gcagcctggg gaggtgaaat tcac 24



<210> 18  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Peptide

<400> 18  
 Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg  
     1                    5                    10

<210> 19  
 <211> 18  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Peptide

<400> 19  
 Phe Ile Thr Cys Gly Gly Gly Tyr Gly Arg Lys Lys Arg Arg Gln Arg  
     1                    5                    10                    15

Arg Arg

<210> 20  
 <211> 27  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Epogen signal peptide

<400> 20  
 Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Leu Ser Leu  
     1                    5                    10                    15

Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly  
                     20                    25

<210> 21  
 <211> 233  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: peptide of Fc fragment

<400> 21  
 Glu Pro Lys Ser Ala Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala  
     1                    5                    10                    15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro  
                     20                    25                    30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val  
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val  
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln  
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln  
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala  
100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro  
115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr  
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser  
145 150 155 160

Asp Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn  
165 170 175

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu  
180 185 190

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val  
195 200 205

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln  
210 215 220

Lys Ser Leu Ser Leu Ser Pro Gly Lys  
225 230

<210> 22  
<211> 644  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (159) .. (641)

<400> 22  
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gaaaataaaa tcaggactcc taacctgctc cagtcagcct gcttcacga ggcctgtcag 120  
tcagtgcccc acctgtgact gagtgtgcag tgcccagc atg tac cag gtg gtt gca 176  
Met Tyr Gln Val Val Ala  
1 5

ttc ttg gca atg gtc atg gga acc cac acc tac agc cac tgg ccc agc 224  
Phe Leu Ala Met Val Met Gly Thr His Thr Tyr Ser His Trp Pro Ser  
10 15 20



Asn Ser Glu Leu Leu Tyr His Asn Gln Thr Val Phe Tyr Arg Arg Pro  
 115 120 125  
 Cys His Gly Glu Lys Gly Thr His Lys Gly Tyr Cys Leu Glu Arg Arg  
 130 135 140  
 Leu Tyr Arg Val Ser Leu Ala Cys Val Cys Val Arg Pro Arg Val Met  
 145 150 155 160  
 Gly

<210> 24  
 <211> 521  
 <212> PRT  
 <213> Homo sapiens

<400> 23  
 Met Ser Leu Val Leu Leu Ser Leu Ala Ala Leu Cys Arg Ser Ala Val  
 1 5 10 15  
 Pro Arg Glu Pro Thr Val Gln Cys Gly Ser Glu Thr Gly Pro Ser Pro  
 20 25 30  
 Glu Trp Met Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp Leu  
 35 40 45  
 Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile  
 50 55 60  
 Leu Met Asn Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu  
 65 70 75 80  
 Leu Lys Ala Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln Ser  
 85 90 95  
 Tyr Ser Cys Val Arg Cys Asn Tyr Thr Glu Ala Phe Gln Thr Gln Ser  
 100 105 110  
 Gly Gly Lys Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val Glu Leu Asn  
 115 120 125  
 Thr Val Tyr Phe Ile Gly Ala His Asn Ile Pro Asn Ala Asn Met Asn  
 130 135 140  
 Glu Asp Gly Pro Ser Met Ser Val Asn Phe Thr Ser Pro Gly Cys Leu  
 145 150 155 160  
 Asp His Ile Met Lys Tyr Lys Lys Lys Cys Val Lys Ala Gly Ser Leu  
 165 170 175  
 Trp Asp Pro Asn Ile Thr Ala Cys Lys Lys Asn Glu Glu Thr Val Glu  
 180 185 190  
 Val Asn Phe Thr Thr Thr Pro Leu Gly Asn Arg Tyr Met Ala Leu Ile  
 195 200 205  
 Gln His Ser Thr Ile Ile Gly Phe Ser Gln Val Phe Glu Pro His Gln  
 210 215 220  
 Lys Lys Gln Thr Arg Ala Ser Val Val Ile Pro Val Thr Gly Asp Ser  
 225 230 235 240

UNRECORDED



Pro	Arg	Glu	Pro	Thr	Val	Gln	Cys	Gly	Ser	Glu	Thr	Gly	Pro	Ser	Pro			
			20					25					30					
Glu	Trp	Met	Leu	Gln	His	Asp	Leu	Ile	Pro	Gly	Asp	Leu	Arg	Asp	Leu			
		35					40					45						
Arg	Val	Glu	Pro	Val	Thr	Thr	Ser	Val	Ala	Thr	Gly	Asp	Tyr	Ser	Ile			
	50					55					60							
Leu	Met	Asn	Val	Ser	Trp	Val	Leu	Arg	Ala	Asp	Ala	Ser	Ile	Arg	Leu			
	65				70					75					80			
Leu	Lys	Ala	Thr	Lys	Ile	Cys	Val	Thr	Gly	Lys	Ser	Asn	Phe	Gln	Ser			
				85					90						95			
Tyr	Ser	Cys	Val	Arg	Leu	Glu	Cys	Ser	Gly	Ala	Ile	Met	Ala	Arg	Cys			
			100					105					110					
Asp	Leu	Asn	Leu	Leu	Gly	Ser	Ser	Asp	Arg	Ser	Ala	Ser	Ala	Ser	Arg			
		115					120					125						
Ala	Ala	Gly	Thr	Ala	Gly	Val	Gly	His	Gln	Thr	Trp	Leu	Ile	Phe	Val			
	130					135					140							
Val	Phe	Val	Glu	Gly	Gly	Phe	Thr	Val	Leu	Leu	Val	Leu	Asn	Ser	Ser			
	145				150					155					160			
Ala	Gln	Ala	Ile	Cys	Leu	Pro	Arg	Leu	Pro	Lys	Val	Leu	Gly	Leu	Gln			
				165					170					175				
Trp	Thr	Phe	Ser	Tyr	Ile	Gly	Phe	Pro	Val	Glu	Leu	Asn	Thr	Val	Tyr			
			180					185					190					
Phe	Ile	Gly	Ala	His	Asn	Ile	Pro	Asn	Ala	Asn	Met	Asn	Glu	Asp	Gly			
		195					200					205						
Pro	Ser	Met	Ser	Val	Asn	Phe	Thr	Ser	Pro	Gly	Cys	Leu	Asp	His	Ile			
		210				215					220							
Met	Lys	Tyr	Lys	Lys	Lys	Cys	Val	Lys	Ala	Gly	Ser	Leu	Trp	Asp	Pro			
					230					235					240			
Asn	Ile	Thr	Ala	Cys	Lys	Lys	Asn	Glu	Glu	Thr	Val	Glu	Val	Asn	Phe			
				245					250					255				
Thr	Thr	Thr	Pro	Leu	Gly	Asn	Arg	Tyr	Met	Ala	Leu	Ile	Gln	His	Ser			
			260					265					270					
Thr	Ile	Ile	Gly	Phe	Ser	Gln	Val	Phe	Glu	Pro	His	Gln	Lys	Lys	Gln			
		275					280					285						
Thr	Arg	Ala	Ser	Val	Val	Ile	Pro	Val	Thr	Gly	Asp	Ser	Glu	Gly	Ala			
		290				295					300							
Thr	Val	Gln	Leu	Thr	Pro	Tyr	Phe	Pro	Thr	Cys	Gly	Ser	Asp	Cys	Ile			
					310					315					320			
Arg	His	Lys	Gly	Thr	Val	Val	Leu	Cys	Pro	Gln	Thr	Gly	Val	Pro	Phe			
				325					330					335				
Pro	Leu	Asp	Asn	Asn	Lys	Ser	Lys	Pro	Gly	Gly	Trp	Leu	Pro	Ala	Ala			
			340					345					350					

109700-460786

Ala Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro  
355 360 365

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys  
370 375 380

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val  
385 390 395 400

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr  
405 410 415

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu  
420 425 430

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His  
435 440 445

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys  
450 455 460

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln  
465 470 475 480

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu  
485 490 495

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro  
500 505 510

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn  
515 520 525

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu  
530 535 540

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val  
545 550 555 560

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln  
565 570 575

Lys Ser Leu Ser Leu Ser Pro Gly Lys  
580 585

<210> 26

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 26

cattttccta catcggttc cctg

24

<210> 27

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

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<400> 27
tgaatctggc ttctttcact gc
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22

[illegible]